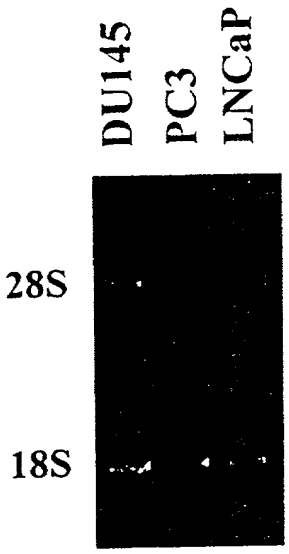


FIG.1A

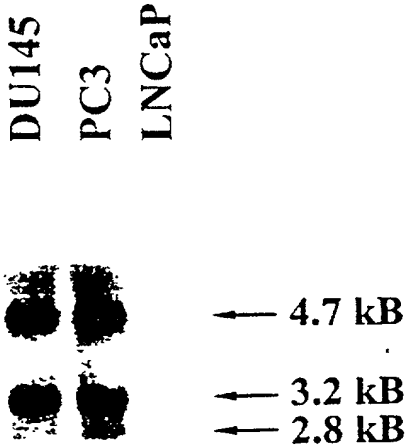


FIG.1B

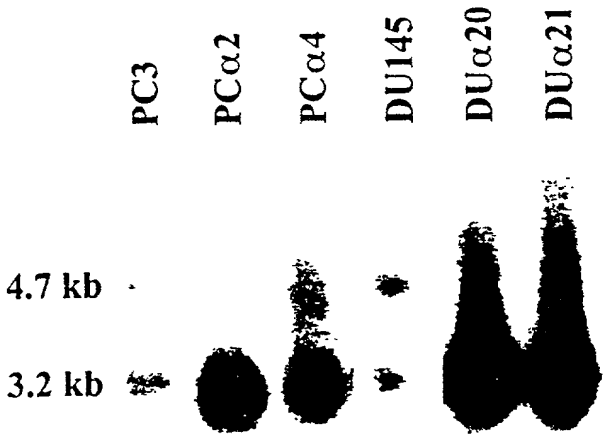
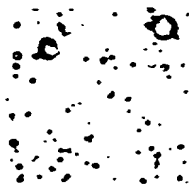


FIG.2



DU145

PC3

DUα20

PCα2

DUα21

PCα4

FIG.3A

FIG.3B

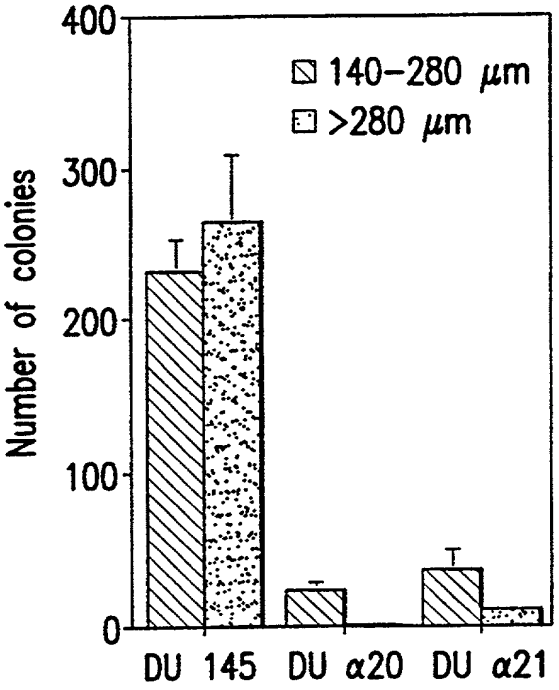


FIG.3A–1

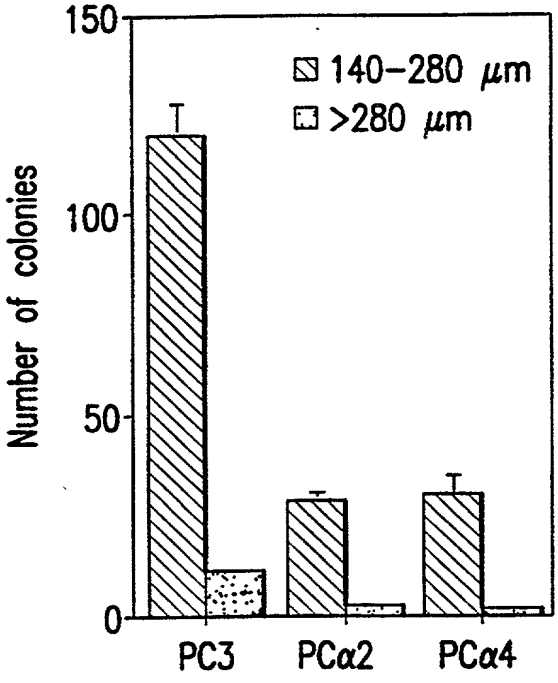


FIG.3B–1

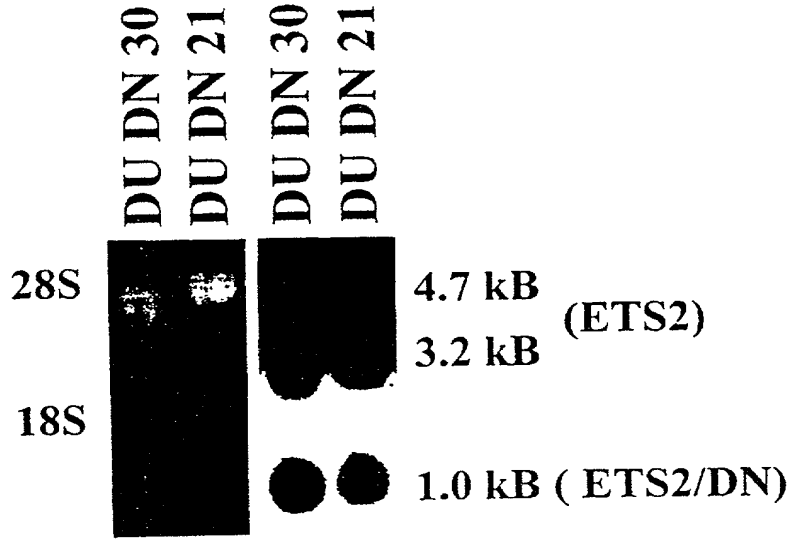

DU DN 30
DU DN 21
DU DN 30
DU DN 21
28S
18S
4.7 kB
3.2 kB
(ETS2)
1.0 kB (ETS2/DN)

FIG.4A

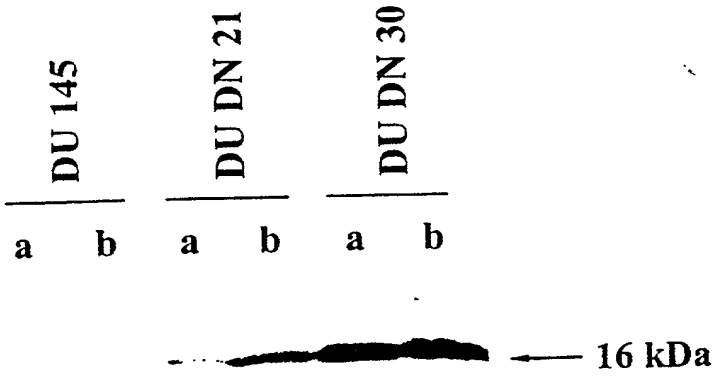

DU 145
DU DN 21
DU DN 30
a b a b a b
16 kDa

FIG.4B

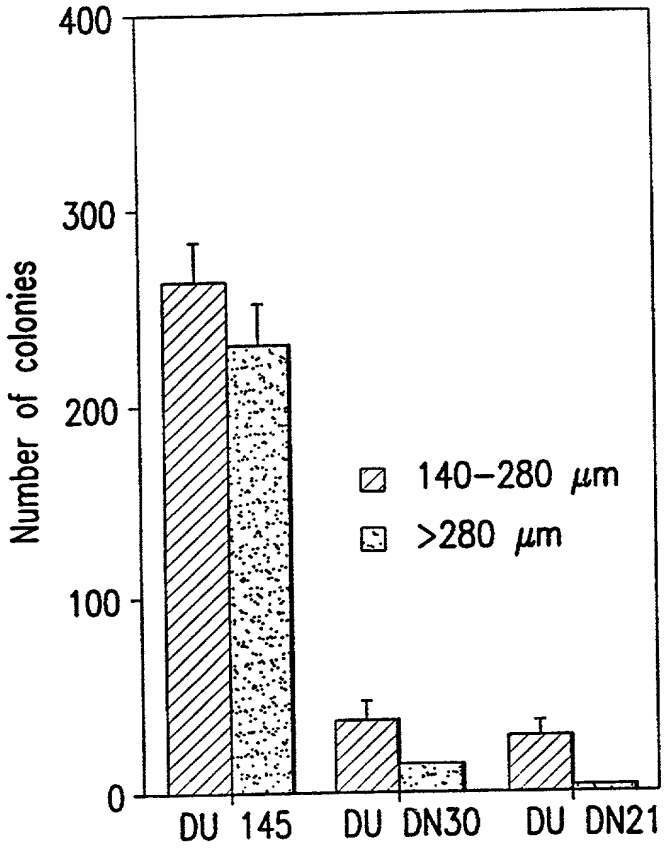

400
300
200
100
0
Number of colonies
140–280 μm
>280 μm
DU 145
DU DN30
DU DN21

FIG.5

```
CCGTTTCCTC CCCTCCCCTC CACTCGGCCG TCCCTCCTTC CTCCTCCCTC CTCCCTCCTC    60
CTCCCGCTCC TGAAGAGCGC GCCGCGTGGG GGACGGCCCG GTTACTTCCT CCAGAGACTG   120
ACGAGTGCGG TGTCGCTCCA GCTCAGAGCT CCCGGAGCCG CCCGGCCAGC GTCCGGCCTC   180
CCTGATCGTC TCTGGCCGGC GCCCTCGCCC TCGCCCGGCG CGCACCGAGC AGCCGCGGGC   240
GCCGAGCAGC CACCGTCCCG ACCAAGCGCC GGCCCTGCCC GCAGCGGCAG GATGAATGAT   300
TTCGGAATCA AGAATATGGA CCAGGTAGCC CCTGTGGCTA ACAGTTACAG AGGGACACTC   360
AAGCGCCAGC CAGCCTTTGA CACCTTTGAT GGGTCCCTGT TTGCTGTTTT TCCTTCTCTA   420
AATGAAGAGC AAACACTGCA AGAAGTGCCA ACAGGCTTGG ATTCCATTTC TCATGACTCC   480
GCCAACTGTG AATTGCCTTT GTTAACCCCG TGCAGCAAGG CTGTGATGAG TCAAGCCTTA   540
AAAGCTACCT TCAGTGGCTT CAAAAAGGAA CAGCGGCGCC TGGGCATTCC AAAGAACCCC   600
TGGCTGTGGA GTGAGCAACA GGTATGCCAG TGGCTTCTCT GGGCCACCAA TGAGTTCAGT   660
CTGGTGAACG TGAATCTGCA GAGGTTCGGC ATGAATGGCC AGATGCTGTG TAACCTTGGC   720
AAGGAACGCT TTCTGGAGCT GGCACCTGAC TTTGTGGGTG ACATTCTCTG GGAACATCTG   780
GAGCAAATGA TCAAAGAAAA CCAAGAAAAG ACAGAAGATC AATATGAAGA AAATTCACAC   840
CTCACCTCCG TTCCTCATTG GATTAACAGC AATACATTAG GTTTTGGCAC AGAGCAGGCG   900
CCCTATGGAA TGCAGACACA GAATTACCCC AAAGGCGGCC TCCTGGACAG CATGTGTCCG   960
GCCTCCACAC CCAGCGTACT CAGCTCTGAG CAGGAGTTTC AGATGTTCCC CAAGTCTCGG  1020
CTCAGCTCCG TCAGCGTCAC CTACTGCTCT GTCAGTCAGG ACTTCCCAGG CAGCAACTTG  1080
AATTTGCTCA CCAACAATTC TGGGACTCCC AAAGACCACG ACTCCCCTGA GAACGGTGCG  1140
GACAGCTTCG AGAGCTCAGA CTCCCTCCTC CAGTCCTGGA ACAGCCAGTC GTCCTTGCTG  1200
GATGTGCAAC GGGTTCCTTC CTTCGAGAGC TTCGAAGATG ACTGCAGCCA GTCTCTCTGC  1260
CTCAATAAGC CAACCATGTC TTTCAAGGAT TACATCCAAG AGAGGAGTGA CCCAGTGGAG  1320
CAAGGCAAAC CAGTTATACC TGCAGCTGTG CTGGCCGGCT TCACAGGAAG TGGACCTATT  1380
CAGCTGTGGC AGTTTCTCCT GGAGCTGCTA TCAGACAAAT CCTGCCAGTC ATTCATCAGC  1440
TGGACTGGAG ACGGATGGGA GTTTAAGCTC GCCGACCCCG ATGAGGTGGC CCGCCGGTGG  1500
GGAAAGAGGA AAAATAAGCC CAAGATGAAC TACGAGAAGC TGAGCCGGGG CTTACGCTAC  1560
TATTACGACA AGAACATCAT CCACAAGACG TCGGGGAAGC GCTACGTGTA CCGCTTCGTG  1620
TGCGACCTCC AGAACTTGCT GGGGTTCACG CCCGAGGAAC TGCACGCCAT CCTGGGCGTC  1680
CAGCCCGACA CGGAGGACTG AGGTCGCCGG GACCACCCTG AGCCGGCCCC AGGCTCGTGG  1740
ACTGAGTGGG AAGCCCATCC TGACCAGCTG CCTCCGAGGA CCCAGGAAAG GCAGGATTGA  1800
AAATGTCCAG GAAAGTGGCC AAGAAGCAGT GGCCTTATTG CATCCCAAAC CACGCCTCTT  1860
GACCAGGCTG CCTCCCTTGT GGCAGCAACG GCACAGCTAA TTCTACTCAC AGTGCTTTTA  1920
AGTGAAAATG GTCGAGAAAG AGGCACCGGG AAGCCGTCCT GGCGCCTGGC AGTCCGTGGG  1980
ACGGGATGGT TCTGGCTGTT TGAGATTCTC AAAGGAGCGA GCATGTCGTG GACACACACA  2040
GACTATTTTT AGATTTTCTT TTGCCTTTTG CAACCAGGAA CAGCAAATGC AAAAACTCTT  2100
TGAGAGGGTA GGAGGGTGGG AAGGAAACAA CCATGTCATT TCAGAAGTTA GTTTGTATAT  2160
ATTATAATAA TCTTATAATT GTTCTCAGAA TCCCTTAACA GTTGTATTTA ACAGAAATTG  2220
TATATTGTAA TTTAAAATAA TTATATAACT GTATTTGAAA TAAGAATTC              2269
```

FIG.6

Met Asn Asp Phe Gly Ile Lys Asn Met Asp Gln Val Ala Pro Val Ala
1 5 10 15
Asn Ser Tyr Arg Gly Thr Leu Lys Arg Gln Pro Ala Phe Asp Thr Phe
20 25 30
Asp Gly Ser Leu Phe Ala Val Phe Pro Ser Leu Asn Glu Glu Gln Thr
35 40 45
Leu Gln Glu Val Pro Thr Gly Leu Asp Ser Ile Ser His Asp Ser Ala
50 55 60
Asn Cys Glu Leu Pro Leu Leu Thr Pro Cys Ser Lys Ala Val Met Ser
65 70 75 80
Gln Ala Leu Lys Ala Thr Phe Ser Gly Phe Lys Lys Glu Gln Arg Arg
85 90 95
Leu Gly Ile Pro Lys Asn Pro Trp Leu Trp Ser Glu Gln Gln Val Cys
100 105 110
Gln Trp Leu Leu Trp Ala Thr Asn Glu Phe Ser Leu Val Asn Val Asn
115 120 125
Leu Gln Arg Phe Gly Met Asn Gly Gln Met Leu Cys Asn Leu Gly Lys
130 135 140
Glu Arg Phe Leu Glu Leu Ala Pro Asp Phe Val Gly Asp Ile Leu Trp
145 150 155 160
Glu His Leu Glu Gln Met Ile Lys Glu Asn Gln Glu Lys Thr Glu Asp
165 170 175
Gln Tyr Glu Glu Asn Ser His Leu Thr Ser Val Pro His Trp Ile Asn
180 185 190
Ser Asn Thr Leu Gly Phe Gly Thr Glu Gln Ala Pro Tyr Gly Met Gln
195 200 205
Thr Gln Asn Tyr Pro Lys Gly Gly Leu Leu Asp Ser Met Cys Pro Ala
210 215 220
Ser Thr Pro Ser Val Leu Ser Ser Glu Gln Glu Phe Gln Met Phe Pro
225 230 235 240
Lys Ser Arg Leu Ser Ser Val Ser Val Thr Tyr Cys Ser Val Ser Gln
245 250 255
Asp Phe Pro Gly Ser Asn Leu Asn Leu Leu Thr Asn Asn Ser Gly Thr
260 265 270
Pro Lys Asp His Asp Ser Pro Glu Asn Gly Ala Asp Ser Phe Glu Ser
275 280 285
Ser Asp Ser Leu Leu Gln Ser Trp Asn Ser Gln Ser Ser Leu Leu Asp
290 295 300
Val Gln Arg Val Pro Ser Phe Glu Ser Phe Glu Asp Asp Cys Ser Gln
305 310 315 320
Ser Leu Cys Leu Asn Lys Pro Thr Met Ser Phe Lys Asp Tyr Ile Gln
325 330 335

```
Glu Arg Ser Asp Pro Val Glu Gln Gly Lys Pro Val Ile Pro Ala Ala
            340                 345                 350
Val Leu Ala Gly Phe Thr Gly Ser Gly Pro Ile Gln Leu Trp Gln Phe
        355                 360                 365
Leu Leu Glu Leu Leu Ser Asp Lys Ser Cys Gln Ser Phe Ile Ser Trp
    370                 375                 380
Thr Gly Asp Gly Trp Glu Phe Lys Leu Ala Asp Pro Asp Glu Val Ala
385                 390                 395                 400
Arg Arg Trp Gly Lys Arg Lys Asn Lys Pro Lys Met Asn Tyr Glu Lys
                405                 410                 415
Leu Ser Arg Gly Leu Arg Tyr Tyr Tyr Asp Lys Asn Ile Ile His Lys
            420                 425                 430
Thr Ser Gly Lys Arg Tyr Val Tyr Arg Phe Val Cys Asp Leu Gln Asn
        435                 440                 445
Leu Leu Gly Phe Thr Pro Glu Glu Leu His Ala Ile Leu Gly Val Gln
    450                 455                 460
Pro Asp Thr Glu Asp
465
```

FIG.7B

```
                    ..**  .* .       * *      *..   .  ... ** .* ..  *.*....*..* *   . . *.   .. .*.*
ETS1 HUMAN  SG-PIQLWQFLLELLTDKS-COSFISWTG-DGWEFKLS--DPDEVARRWGKRK-WEPKMNYEKLSRGLRYYYDKNIIRKTA-GKRYVYRFV-
ETS1 MOUSE  SG-PIQLWQFLLELLTDKS-COSFISWTG-DGWEFKLS--DPDEVARRWGKRK-WEPKMNYEKLSRGLRYYYDKNIIRKTA-GKRYVYRFV-
ETSB CHICK  SG-PIQLWQFLLELLTDKS-COSFISWTG-DGWEFKLS--DPDEVARRWGKRK-WEPKMNYEKLSRGLRYYYDKNIIRKTA-GKRYVYRFV-
ETSA XENLA  SG-PIQLWQFLLELLTDKS-COSFISWTG-DGWEFKLS--DPDEVARRWGKRK-WEPKMNYEKLSRGLRYYYDKNIIRKTA-GKRYVYRFV-
vETS E26    SG-PIQLWQFLLELLTDKS-COSFISWTG-DGWEFKLS--DPDEVARRWGKRK-WEPKMNYEKLSRGLRYYYDKNIIRKTA-GKRYVYRFV-
ETS2 XENLA  SG-PIQLWQFLLELLTDKS-COSFISWTG-DGWEFKLS--DPDEVARRWGKRK-WEPKMNYEKLSRGLRYYYDKNIIRKTA-GKRYVYRFV-
ETS2 HUMAN  SG-PIQLWQFLLELLTDKS-COSFISWTG-DGWEFKLS--DPDEVARRWGKRK-WEPKMNYEKLSRGLRYYYDKNIIRKTA-GKRYVYRFV-
ETS2 MOUSE  SG-PIQLWQFLLELLTDKS-COSFISWTG-DGWEFKLS--DPDEVARRWGKRK-WEPKMNYEKLSRGLRYYYDKNIIRKTA-GKRYVYRFV-
ETS2 CHICK  SG-PIQLWQFLLELLTDKS-COSFISWTG-DGWEFKLS--DPDEVARRWGRRK-WEPKMNYEKLSRGLRYYYDKNIIRKTA-GKRYVYRFV-
ETS2 SEAUR  SG-PIQLWQFLLELLTDKS-COSFISWTG-DGWEFKLS--DPDEVARRWGKRK-WEPKMNYEKLSRGLRYYYDKNIIRKTA-GKRYVYRFV-
ETS2 DROME  SG-PIQLWQFLLELLTDKS-COSFISWTG-DGWEFKLS--DPDEVARRWGIRK-WEPKMNYEKLSRGLRYYYDKNIIRKTA-GKRYVYRFV-
FLI1 MOUSE  SG-QIQLWQFLLELLSDSA-NASCITWEG-TNGEFKMT--DPDEVARRWGERK-SKPNMNYDKLSRALRYYYDKNIMTKVH-GKRYAYKFD-
ERG  HUMAN  SG-QIQLWQFLLELLSDSS-NASCITWEG-TNGEFKMT--DPDEVARRWGERK-SKPNMNYDKLSRALRYYYDKNIMTKVH-GKRYAYKFD-
ETS3 DROME  GSGQIQ WQPLLELLSDSN-NASCITWEGTNG EFKLT--DPDEVARRWGERK-SKPNMNTDKLSRALR
ETS6 DROME  SGGQIQLWQPLLELLADSS-NANAISWEG-QSGEFRLI--DPDEVARRWGERK-AKPNMNYDKLSRALRYYYDKNIMTEVH-GKRYAYKFD-
GABP RAT    NG-QIQLWQFLLELLTDKD-ARDCISWVG-DEGEFKLN--QPELVAQKWGQRK-NKPTMNYPKLSRALRYYYDGDMICKVQ-GKGFVYKFV-
DELG DROME  NG-QVQLWQFLLEILTDCE-HTDVIEWVG-TEGEFKLT--DPDRVARLWGEKK-NKPTMNYPKLSRALRYYYDGDMISKVS-GQKFVYKFV-
PEA3 MOUSE  RGA-LQLWQFLVALLDDPT-NARFLAWTG-RQMEFKLI--EPEEVARLWGIQK-NRPAMNYDKLSRSLRYYYEKGIMQKVA-GERYVYKFV-
ELK  HUMAN  MDPSVTLWQFLLQLLREQG-NGHIISNTSRDGGEFKLV--DAEEVARLWGLRK-NKTNMNTDKLSRALRYYYQKNIIRKVS-GQKFVYKFV-
SAP1 HUMAN  MDSAITLWQFLLQLLQKPQ-NKHMICWTSNDG-QFKLL--QAEEVARLWGIRK-NKPNMNYDKLSRALRYYYVKNIIKKVN-GQKVYKFVS-
ELKX MOUSE        LWQFLLLLLLDQN-HDHLICNTSNDG-QFKLL--KAEEVAKLWGLRK-NETNMNYDKLSRALR
ELF1 HUMAN  KGNTIYLWEFLLALLQDKATCPKYIKWTQREKGIFKLV--DSKAVSRLWGKHK-NKEDMNYETMGRALRYYYQRGILAKVE-GQRLVIQFK
E74A DROME  EGSTTYLWEFLLKLLQDREYCPRFIKWTNREKGVFKLV--DSKAVSRLWGMHK-NKEDMNYETMGRALRYYYQRGILAKVD-GQRLVIHFV
ETS4 DROME  GGSHIHLWQFLKELLASPQVNGTAIRWIDRSKGIPKIE--DSVRVAKLWGRRK-NRPAMNYDKLLRSIRQYYKKGIMKKSERSQRLVYQFC
PU1  MOUSE  SKKKIRLYQFLLDLLRSGDM-KDSIWWVDKDKGTFQFSSKHKEALAHRWGIQKGNRKKNTYQKMARALRNYGKTGEVKKVK--KKLTYQF-S
PU1  HUMAN  SKKKIRLYQFLLDLLRSGDM-KDSIWWVDKDKGTFQFSSKHKEALAHRWGIQKGNRKKNTYQKMARALRNYGKTGEVKKVK--KKLTYQF-S
```

FIG.8A

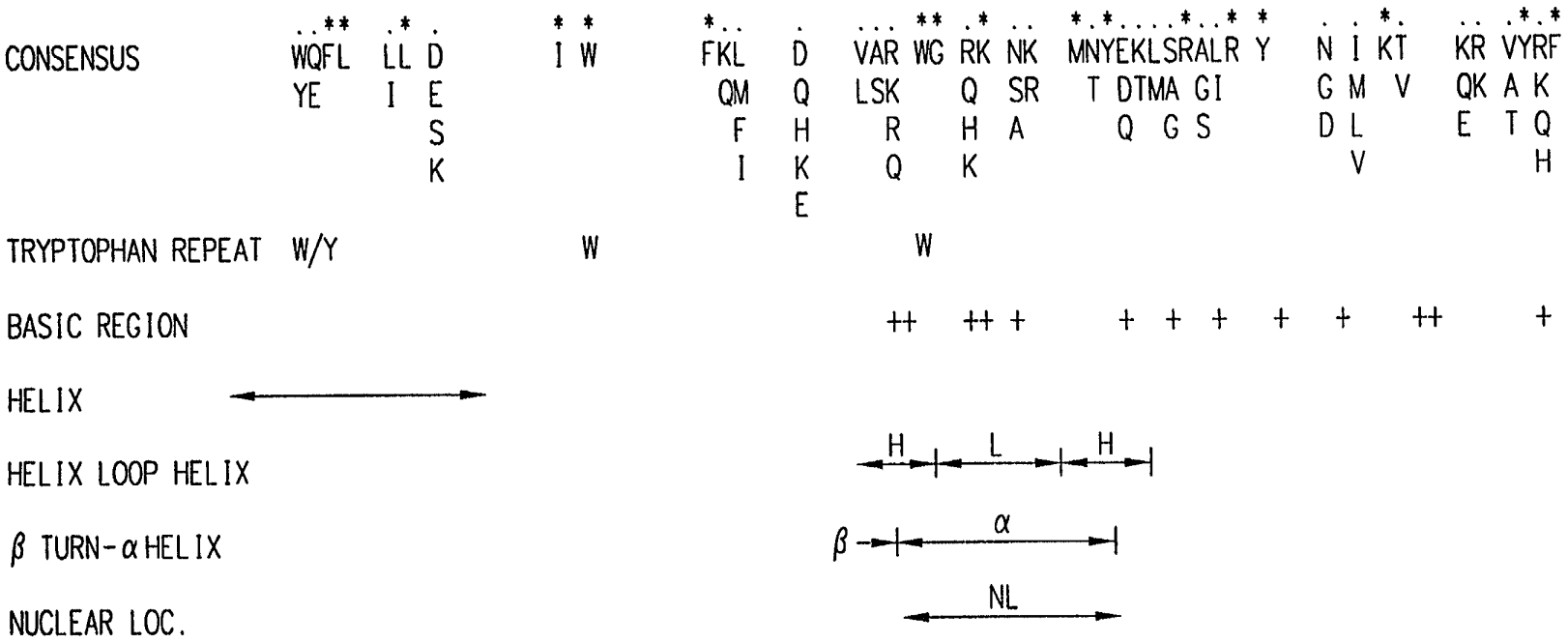


FIG.8B

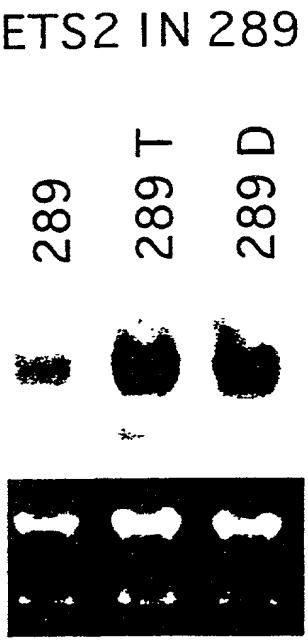


FIG.9A

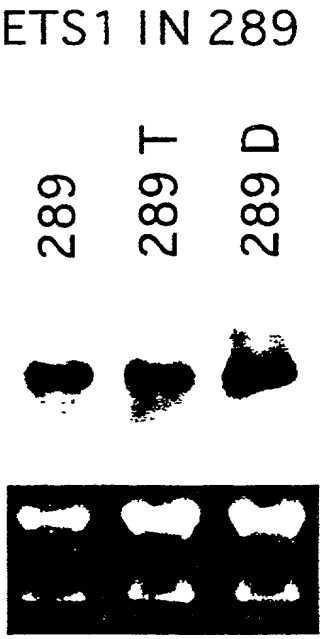


FIG.9B

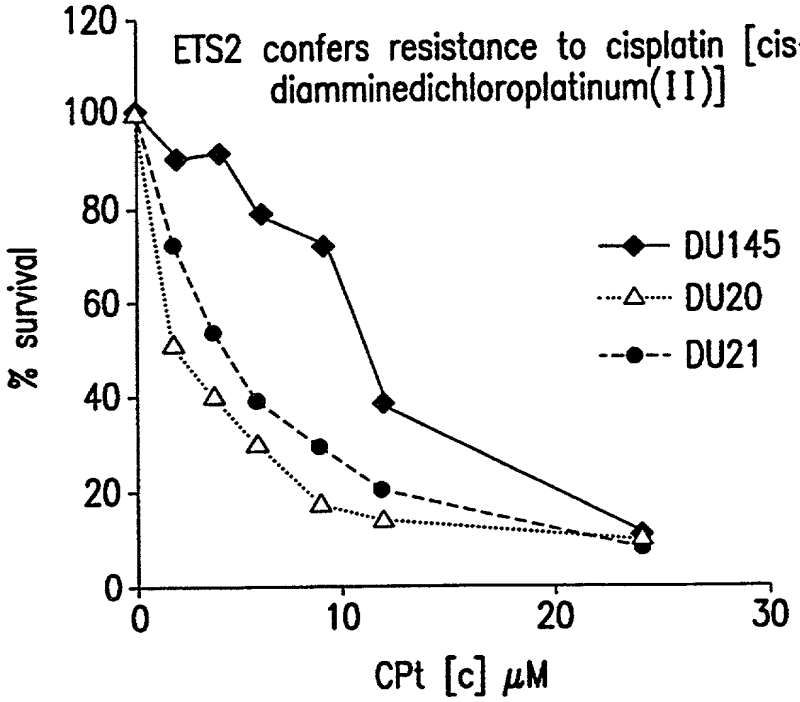

ETS2 confers resistance to cisplatin [cis-diamminedichloroplatinum(II)]
% survival
120
100
80
60
40
20
0
0
10
20
30
CPt [c] μM
DU145
DU20
DU21

FIG.10